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AMENDMENTS

In the abstract:

Methods are provided for identifying heterogeneous features, including heterogeneous background regions, in an image of an array, e.g., in an image of a biopolymeric array, such as a nucleic acid array. The subject methods employ an algorithm that employs a different dispersity measure depending on whether the signal features are weaker or stronger. In the subject methods, a toggle parameter, e.g., a single value (i.e., toggle point) or range of values (i.e., toggle range, smooth function), for the array of features is first determined. The toggle parameter is determined using statistics obtained from low signal features on the array. Following determination of the toggle parameter, those features that have a signal intensity that is either: (a) equal to or less than the toggle parameter and have an intra-feature noise metric-1 level, e.g., standard deviation, that exceeds the intra-feature noise limit for metric-1; or (b) greater than the toggle point and have an intra-feature noise metric-2 level that exceeds the intra-feature noise limit for metric-2, e.g., coefficient of variation, are identified as heterogeneous. Also provided are computer readable storage media that include an algorithm capable of performing the steps of the subject methods. The subject methods find use in the processing of images obtained from a variety of different types of arrays, including nucleic acid arrays.